

SEARCH REQUEST FORM

Scientific and Technical Information Center

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 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

Searcher: P. Schreber

Searcher Phone #: 308-4252

Searcher Location: CM1 12C14

Date Searcher Provided: _____

Date Completed: 12/10

Searcher Prep & Review Time: 25

Client Prep Time: _____

Printing Time: 7

Type of Search

NA Sequence (#) 7

AA Sequence (#) 1

Structure (#) _____

Bibliographic _____

Litigation _____

Fulltext: _____

Patent Family _____

Other: _____

Vendors and cost where applicable

STN: _____

Dialog: _____

Questel Orbit: _____

Dr. Link: _____

Lexis Nexis: _____

Sequence Systems: CompuGen

WVAW Internet: _____

Other: _____

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PT DNA coding for aromatic acyl transferase - for transforming plants
PT which produce anthocyanin pigments and thus altering colour tone,
e.g. of flowers
XX
PS Claim 2: Page 81: 94pp: Japanese.
XX
CC Vectors containing DNA fragments encoding proteins of plant origin
CC with aromatic acyl transferase activity may be used to transform
CC plants which produce anthocyanin pigments. The aromatic acyl
CC transferase acylates the pigments in the flower resulting in colour
CC tone changes and allowing new colourations to be produced. Six
CC specific DNA sequences encoding aromatic acyl transferase from
CC different plants are described in AAT37308-737313. This peptide
CC fragment was isolated from three of the six clones and was used to
CC synthesise a degenerate primer (AAT37314) which was then used to
CC identify other aromatic acyl transferase encoding clones.
SQ Sequence 6 AA:

Query Match 100.0%; Score 40; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWGK 6
111111
Db 1 dfgwgk 6

RESULT 2
AAE00248
ID AAE00248 standard: peptide; 7 AA.
XX
AC AAE00248;
XX
DT 13-JUN-2001 (first entry)
XX
DE Peptide fragment #3 to construct degenerate reverse PCR primer AT-REV1.
XX
KM Transacylase: taxol; pacilitaxel biosynthesis; taxoid;
KM transgenic organism.
XX
OS Unidentified.
XX
PN WO200123586-A2.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-US27006.
XX
PR 30-SEP-1999; 99US-0411145.
PR 07-DEC-1999; 99US-0457046.
XX
PA (UNITM) UNITV WASHINGTON STATE RES FOUND.
XX
XX Croteau RB, Walker KD, Schoendorf A, Wildung MR;
PI WPI: 2001-245004/25.
XX
DR New transacylase enzymes, useful for the high yield production of
XX Taxol(TM), related taxoids and useful intermediates in the in the
PT pacilitaxel biosynthetic pathway -
PT
XX
XX
PS Disclosure: Page 40; 162pp; English.
XX
CC The present sequence is a peptide fragment used for constructing
CC degenerate reverse PCR primer AT-REV1. The primers are useful for
CC generating probes which are useful for the identification of
CC (nucleic acid sequences encoding) transacylases. The probes
CC isolated from the Taxus genus are useful for the synthetic production
CC of Taxol(TM) and related taxoids, as well as intermediates in the
CC pacilitaxel biosynthetic pathway. They can also be used for the creation
CC of transgenic organisms that either produce the transacylases for

CC subsequent in vitro use, or produce the transacylases in vivo. The
CC (nucleic acids encoding) transacylases are also useful for creating
CC specific binding agents that recognise the corresponding transacylases.
CC Binding agents include (fragments of) antibodies or any other agent
CC capable of specifically binding to the groups on the proteins.
XX
SQ Sequence 7 AA:

Query Match 100.0%; Score 40; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 dfgwgk 6

RESULT 3
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ID AAG07709 standard: Protein; 287 AA.
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AC AAG07709;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4964.
XX
KM Protein identification: signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
XX Arabidopsis thaliana.
XX
OS EPI033405-A2.
XX
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XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
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Query Match 100.0%; Score 40; DB 21; Length 287;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DEFGMK 6
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Db 229 dfgwqk 234

RESULT 4
AAG49296
ID AAG49296 standard; Protein: 287 AA.
XX
AC AAG49296;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 62350.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hydridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX Arabidopsis thaliana.
OS
PM EPI033405-A2.
XX
PD 06-SEP-2000.
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PE 25-FEB-2000; 2000EP-0301439.
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Query Match 100.0%; Score 40; DB 21; Length 287;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRGWCK 6

Db 229 dfgwck 234
RESULT 5
ID AG07708
ID AG07708 standard; Protein: 293 AA.
AC AG07708;
AC AG07708;
DT 17-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4963.
DE Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
XX EP103405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 200EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0123180.
XX PR 09-MAR-1999; 99US-0123548.
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XX PR 29-MAR-1999; 99US-0126785.
XX PR 01-APR-1999; 99US-0127462.
XX PR 06-APR-1999; 99US-0128234.
XX PR 08-APR-1999; 99US-0128714.
XX PR 16-APR-1999; 99US-0128845.
XX PR 19-APR-1999; 99US-0130077.
XX PR 21-APR-1999; 99US-0130449.
XX PR 23-APR-1999; 99US-0130510.
XX PR 28-APR-1999; 99US-0130891.
XX PR 30-APR-1999; 99US-0131449.
XX PR 30-APR-1999; 99US-0132048.
XX PR 04-MAY-1999; 99US-0132407.
XX PR 04-MAY-1999; 99US-0132484.
XX PR 05-MAY-1999; 99US-0132485.
XX PR 06-MAY-1999; 99US-0132486.
XX PR 07-MAY-1999; 99US-0132487.
XX PR 11-MAY-1999; 99US-0132863.
XX PR 14-MAY-1999; 99US-0134216.
XX PR 14-MAY-1999; 99US-0134219.
XX PR 14-MAY-1999; 99US-0134221.
XX PR 14-MAY-1999; 99US-0134221.
XX PR 14-MAY-1999; 99US-0134370.
XX PR 18-MAY-1999; 99US-0134768.
XX PR 19-MAY-1999; 99US-0134941.
XX PR 20-MAY-1999; 99US-0135124.
XX PR 21-MAY-1999; 99US-0135353.
XX PR 24-MAY-1999; 99US-0135629.
XX PR 25-MAY-1999; 99US-0136021.
XX PR 27-MAY-1999; 99US-0136392.
XX PR 28-MAY-1999; 99US-0136782.
XX PR 01-JUN-1999; 99US-0137222.
XX PR 03-JUN-1999; 99US-0137528.
XX PR 04-JUN-1999; 99US-0137502.
XX PR 07-JUN-1999; 99US-0137724.
XX PR 08-JUN-1999; 99US-0138094.
XX PR 10-JUN-1999; 99US-0138540.
XX PR 10-JUN-1999; 99US-0138847.
XX PR 14-JUN-1999; 99US-0139119.
XX PR 16-JUN-1999; 99US-0139452.
XX PR 17-JUN-1999; 99US-0139453.
XX PR 18-JUN-1999; 99US-0139454.


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XX AAC49295;
AC
XX 18-OCT-2000 (first entry)
DT
XX Arabidopsis thaliana protein fragment SEQ ID NO: 62349.
DE
XX Arabidopsis thaliana protein fragment SEQ ID NO: 62349.
XX Protein identification: signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
OS Arabidopsis thaliana.
XX
XX EP1033405-A2.
PN
XX 06-SEP-2000.
PD
XX
XX 25-FEB-2000; 2000EP-0301439.
PF
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
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PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
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PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
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PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
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PR 14-JUN-1999; 99US-0139119.
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PR 17-JUN-1999; 99US-0139492.
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PR 18-JUN-1999; 99US-0139460.
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PR 18-JUN-1999; 99US-0139750.
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PR 22-JUN-1999; 99US-0139899.
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PR 23-JUN-1999; 99US-0140354.
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PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
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PR 22-JUL-1999; 99US-0145085.
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PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
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PR 12-AUG-1999; 99US-0148341.
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PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
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PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
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PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
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PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 14-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
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PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161921.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match      100.0%; Score 40; DB 21; Length 293;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DFGWGK 6
DB 235 dfgwgk 240

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RESULT 7
AAE00230
ID AAE00230 standard; Protein; 302 AA.
AC
XX
XX AAE00230;
XX
DT 13-JUN-2001 (first entry)
XX
DE Protein encoded by Probe 4.
XX

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KW Transacylase; taxol; paclitaxel biosynthesis; taxold; probe;
KM transgenic organism.
XX
XX Taxus cuspidata.
OS
XX WO200123586-A2.
XX
XX 05-APR-2001.
PD
XX
XX 29-SEP-2000; 2000WO-US27006.
XX
XX 30-SEP-1999; 99US-0411145.
PR 07-DEC-1999; 99US-0457046.
XX
XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.
XX
XX Croteau RB, Walker KD, Schoendorf A, Wildung MR;
XX WPI; 2001-245004/25.
XX N-PSDB; AAD03336.
XX
XX New transacylase enzymes, useful for the high yield production of
PT Taxol(TM), related taxoids and useful intermediates in the in the
PT paclitaxel biosynthetic pathway
XX
XX Claim 1; Page 101-102; 162pp; English.
XX
XX The present sequence is the amino acid sequence of probe 4. Probe 4
CC is derived from AT-FOR3 and AT-REV1 primers and is used for screening
CC Taxus cuspidata transacylase cDNA. The probes are useful for the
CC identification of (nucleic acid sequences encoding) transacylases.
CC The probes isolated from the Taxus genus are useful for the
CC synthetic production of Taxol(TM) and related taxoids, as well as
CC intermediates in the paclitaxel biosynthetic pathway. They can also
CC be used for the creation of transgenic organisms that either produce
CC the transacylases for subsequent in vitro use, or produce the
CC transacylases in vivo. The (nucleic acids encoding) transacylases are
CC also useful for creating specific binding agents that recognise the
CC corresponding transacylases. Binding agents include (fragments of)
CC antibodies or any other agent capable of specifically binding to the
CC groups on the proteins.
XX
XX Sequence 302 AA;
SQ

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Query Match      100.0%; Score 40; DB 22; Length 302;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DFGWGK 6
DB 297 dfgwgk 302

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RESULT 8
AAE00231
ID AAE00231 standard; Protein; 302 AA.
AC
XX
XX AAE00231;
XX
DT 13-JUN-2001 (first entry)
XX
DE Protein encoded by Probe 5.
XX
XX Transacylase; taxol; paclitaxel biosynthesis; taxold; probe;
KM transgenic organism; TAX5.
XX
XX Taxus cuspidata.
XX
XX WO200123586-A2.
XX
XX 05-APR-2001.
XX

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DR WPI: 2001-245004/25.
DR N-PSDB: AAD03341.
XX New transacylase enzymes, useful for the high yield production of
PT Taxol(TM), related taxoids and useful intermediates in the in the
PT pacitaxel biosynthetic pathway -
XX
PS Claim 1: Page 108-109; 162pp; English.
XX
CC The present sequence is the amino acid sequence of probe 9.
CC Probe 9 is derived from AT-FOR2 and AT-REVI primers and is
CC used for screening Taxus cuspidata TAX9 full length cDNA clone. The
CC probes are useful for the identification of (nucleic acid sequences
CC encoding) transacylases. The probes isolated from the Taxus genus
CC are useful for the synthetic production of Taxol(TM) and related taxoids,
CC as well as intermediates in the pacitaxel biosynthetic pathway. They
CC can also be used for the creation of transgenic organisms that either
CC produce the transacylases for subsequent in vitro use, or produce the
CC transacylases in vivo. The (nucleic acids encoding) transacylases are
CC also useful for creating specific binding agents that recognise the
CC corresponding transacylases. Binding agents include (fragments of)
CC antibodies or any other agent capable of specifically binding to the
CC groups on the proteins.
XX
SQ Sequence 302 AA;

Query Match 100.0%; Score 40; DB 22; Length 302;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPGWCK 6
|11111
Db 297 dfgwck 302

RESULT 11

AAE00238
ID AAE00238 standard; Protein: 302 AA.

XX AAE00238;

DT 13-JUN-2001 (first entry)

XX Protein encoded by Probe 12.

XX Transacylase; taxol; pacitaxel biosynthesis; taxoid; probe;

KW transgenic organism; TAX12.

XX Taxus cuspidata.

OS WO200123586-A2.

XX 05-APR-2001.

PD 29-SEP-2000; 2000WO-US27006.

XX 30-SEP-1999; 99US-0411145.

PR 07-DEC-1999; 99US-0457046.

XX (UNIM) UNIV WASHINGTON STATE RES FOUND.

PA Croteau RB, Walker KD, Schoendorf A, Wildung MR;

XX WPI: 2001-245004/25.

DR N-PSDB: AAD03344.

XX New transacylase enzymes, useful for the high yield production of
PT Taxol(TM), related taxoids and useful intermediates in the in the
PT pacitaxel biosynthetic pathway -
XX
PS Claim 1: Page 113; 162pp; English.

CC The present sequence is the amino acid sequence of probe 12. Probe 12
CC is derived from AT-FOR3 and AT-REVI primers and is used for screening
CC Taxus cuspidata TAX12 full length cDNA clone. The probes are useful for
CC the identification of (nucleic acid sequences encoding) transacylases.
CC The probes isolated from the Taxus genus are useful for the
CC synthetic production of Taxol(TM) and related taxoids, as well as
CC intermediates in the pacitaxel biosynthetic pathway. They can also
CC be used for the creation of transgenic organisms that either
CC produce the transacylases for subsequent in vitro use, or produce the
CC transacylases in vivo. The (nucleic acids encoding) transacylases are
CC also useful for creating specific binding agents that recognise the
CC corresponding transacylases. Binding agents include (fragments of)
CC antibodies or any other agent capable of specifically binding to the
CC groups on the proteins.
XX
SQ Sequence 302 AA;

Query Match 100.0%; Score 40; DB 22; Length 302;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPGWCK 6
|11111
Db 297 dfgwck 302

RESULT 12

AAE00232
ID AAE00232 standard; Protein: 303 AA.

XX AAE00232;

DT 13-JUN-2001 (first entry)

XX Protein encoded by Probe 6.

XX Transacylase; taxol; pacitaxel biosynthesis; transgenic organism; TAX6;

KW (10-deacetyl)baccalin III-0-O-acetyltransferase); taxoid; probe.

XX Taxus cuspidata.

OS WO200123586-A2.

XX 05-APR-2001.

PD 29-SEP-2000; 2000WO-US27006.

XX 30-SEP-1999; 99US-0411145.

PR 07-DEC-1999; 99US-0457046.

XX (UNIM) UNIV WASHINGTON STATE RES FOUND.

PA Croteau RB, Walker KD, Schoendorf A, Wildung MR;

XX WPI: 2001-245004/25.

DR N-PSDB: AAD03338.

XX New transacylase enzymes, useful for the high yield production of
PT Taxol(TM), related taxoids and useful intermediates in the in the
PT pacitaxel biosynthetic pathway -
XX
PS Claim 1: Page 104-105; 162pp; English.
XX
CC The present sequence is the amino acid sequence of probe 6.
CC Probe 6 is derived from AT-FOR2 and AT-REVI primers and is
CC used for screening Taxus cuspidata full length cDNA clone
CC TAX6 (10-deacetyl)baccalin III-0-O-acetyl transferase). The
CC probes are useful for the identification of (nucleic acid sequences
CC encoding) transacylases. The probes isolated from the Taxus genus
CC are useful for the synthetic production of Taxol(TM) and related taxoids,
CC as well as intermediates in the pacitaxel biosynthetic pathway. They
CC can also be used for the creation of transgenic organisms that either

CC produce the transacylases for subsequent in vitro use, or produce the
CC transacylases in vivo. The (nucleic acids encoding) transacylases are
CC also useful for creating specific binding agents that recognise the
CC corresponding transacylases. Binding agents include (fragments of)
CC antibodies or any other agent capable of specifically binding to the
CC groups on the proteins.

XX Sequence 303 AA:

Query Match 100.0%; Score 40; DB 22; Length 303;

Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWGK 6
|||||
Db 298 dfwgk 303

RESULT 13

AAE00236
ID AAE00236 standard; Protein: 303 AA.

XX
AC AAE00236;

XX 13-JUN-2001 (first entry)

XX Protein encoded by Probe 10.

DE Transacylase; taxol; paciltaxel biosynthesis; taxoid; probe;

XX Transgenic organism; TAX10.

XX Taxus cuspidata.

XX WO200123586-A2.

XX 05-APR-2001.

XX 29-SEP-2000; 2000WO-US27006.

XX 30-SEP-1999; 99US-0411145.

XX 07-DEC-1999; 99US-0457046.

PA (UNITW) UNIV WASHINGTON STATE RES FOUND.

PI Croteau RB, Walker KD, Schoendorf A, Wildung MR;

XX WPI: 2001-245004/25.

DR N-PSDB: AAD03342.

PT New transacylase enzymes, useful for the high yield production of
PT Taxol(TM), related taxoids and useful intermediates in the in the
PT paciltaxel biosynthetic pathway -

XX Claim 1; Page 110-111; 162pp; English.

XX The present sequence is the amino acid sequence of probe 10.

XX Probe 10 is derived from AT-FOR4 and AT-REV1 primers is used
XX for screening Taxus cuspidata TAX10 full length cDNA clone. The

XX probes are useful for the identification of (nucleic acid sequences
XX encoding) transacylases. The probes isolated from the Taxus genus

XX are useful for the synthetic production of Taxol(TM) and related taxoids,
XX as well as intermediates in the paciltaxel biosynthetic pathway. They

XX can also be used for the creation of transgenic organisms that either
XX produce the transacylases for subsequent in vitro use, or produce the

XX transacylases in vivo. The (nucleic acids encoding) transacylases are
XX also useful for creating specific binding agents that recognise the

XX corresponding transacylases. Binding agents include (fragments of)
XX antibodies or any other agent capable of specifically binding to the
XX groups on the proteins.

SO Sequence 303 AA:

Query Match 100.0%; Score 40; DB 22; Length 303;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWGK 6
|||||
Db 298 dfwgk 303

RESULT 14

AAE00227
ID AAE00227 standard; Protein: 306 AA.

XX
AC AAE00227;

XX 13-JUN-2001 (first entry)

XX Protein encoded by Probe 1.

DE TAX1; taxadien-5 alpha-ol acetyl transferase; transacylase; taxol;

XX TAX2; taxadien-2 alpha-O-benzoyl transferase; paciltaxel biosynthesis;

XX taxoid; Transgenic organism; probe.

XX Taxus cuspidata.

XX WO200123586-A2.

XX 05-APR-2001.

XX 29-SEP-2000; 2000WO-US27006.

XX 30-SEP-1999; 99US-0411145.

XX 07-DEC-1999; 99US-0457046.

PA (UNITW) UNIV WASHINGTON STATE RES FOUND.

PI Croteau RB, Walker KD, Schoendorf A, Wildung MR;

XX WPI: 2001-245004/25.

DR N-PSDB: AAD03333.

PT New transacylase enzymes, useful for the high yield production of
PT Taxol(TM), related taxoids and useful intermediates in the in the
PT paciltaxel biosynthetic pathway -

XX Claim 1; Page 96-97; 162pp; English.

XX The present sequence is the amino acid sequence of probe 1. Probe 1 is
XX derived from AT-FOR1 and AT-REV1 primers and is used for screening

XX Taxus cuspidata full length cDNA clones TAX1 or TAX01 (taxadien-5 alpha-
XX ol acetyl transferase) and TAX2 or TAX02 (taxadien-2 alpha-O-benzoyl

XX acid sequences encoding) transacylases. The probes isolated from
XX the Taxus genus are useful for the synthetic production of (nucleic

XX acid sequences encoding) transacylases. The probes isolated from
XX the Taxus genus are useful for the synthetic production of Taxol(TM) and

XX related taxoids, as well as intermediates in the paciltaxel biosynthetic
XX pathway. They can also be used for the creation of transgenic organisms

XX that either produce the transacylases for subsequent in vitro use, or
XX produce the transacylases in vivo. The (nucleic acids encoding)

XX transacylases are also useful for creating specific binding agents that
XX recognise the corresponding transacylases. Binding agents include
XX (fragments of) antibodies or any other agent capable of specifically

XX binding to the groups on the proteins.

SO Sequence 306 AA:

Query Match 100.0%; Score 40; DB 22; Length 306;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWGK 6
|||||

Db 301 dfgwqk 306

RESULT 15

AAE00228

ID AAE00228 standard; Protein: 306 AA.

XX AAE00228;

XX 13-JUN-2001 (first entry)

DE Protein encoded by Probe 2.

XX TAX2; taxadien-2 alpha-O-benzoyl transferase; pacilitaxel biosynthesis;

KW taxold; transgenic organism; probe; transacylase; taxol.

XX Taxus cuspidata.

OS WO200123586-A2.

XX 05-APR-2001.

XX 29-SEP-2000; 2000WO-US27006.

XX 30-SEP-1999; 99US-0411145.

XX 07-DEC-1999; 99US-0457046.

XX (UNIW) UNIV WASHINGTON STATE RES FOUND.

XX Croteau RR, Walker KD, Schoendorf A, Wildung MR;

XX WPI; 2001-245004/25.

XX N-PSDB; AAD03334.

XX New transacylase enzymes, useful for the high yield production of
PT Taxol(TM), related taxoids and useful intermediates in the in the
PT pacilitaxel biosynthetic pathway -

PS Claim 1: Page 98-99; 162pp; English.

XX The present sequence is the amino acid sequence of probe 2. Probe 2
CC is used for screening Taxus cuspidata transacylase cDNA. Probe 2
CC is derived from AT-FOR1 and AT-REV1 primers but it is not useful
CC for screening TAX2 or TAX02 (taxadien-2 alpha-O-benzoyl
CC transferase) but has the sequence similar to TAX2 gene. The
CC probes are useful for the identification of (nucleic acid sequences
CC encoding) transacylases. The probes isolated from the Taxus genus
CC are useful for the synthetic production of Taxol(TM) and related taxoids,
CC as well as intermediates in the pacilitaxel biosynthetic pathway. They
CC can also be used for the creation of transgenic organisms that either
CC produce the transacylases for subsequent in vitro use, or produce the
CC transacylases in vivo. The (nucleic acids encoding) transacylases are
CC also useful for creating specific binding agents that recognise the
CC corresponding transacylases. Binding agents include (fragments of)
CC antibodies or any other agent capable of specifically binding to the
CC groups on the proteins.

XX Sequence 306 AA;

Query Match 100.0%; Score 40; DB 22; Length 306;

Best Local Similarity 100.0%; Pred. NO. 27;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGWGK 6

Db 301 dfgwqk 306

Search completed: November 5, 2001, 12:57:31
job time: 33 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 5, 2001, 12:56:59 ; Search time 12.47 seconds
(without alignments)
10.828 Million cell updates/sec

Title: US-08-894-356C-21

Perfect score: 40

Sequence: 1 DFGWGK 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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3: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	7	4	US-09-457-046B-41
2	40	100.0	302	4	US-09-457-046B-8
3	40	100.0	302	4	US-09-457-046B-10
4	40	100.0	302	4	US-09-457-046B-16
5	40	100.0	302	4	US-09-457-046B-18
6	40	100.0	302	4	US-09-457-046B-24
7	40	100.0	303	4	US-09-457-046B-12
8	40	100.0	303	4	US-09-457-046B-20
9	40	100.0	306	4	US-09-457-046B-2
10	40	100.0	306	4	US-09-457-046B-4
11	40	100.0	306	4	US-09-457-046B-22
12	40	100.0	322	4	US-09-457-046B-14
13	40	100.0	331	4	US-09-457-046B-59
14	40	100.0	436	4	US-09-457-046B-62
15	40	100.0	439	4	US-09-457-046B-68
16	40	100.0	448	1	US-08-207-904-2
17	40	100.0	448	1	US-08-207-904-17
18	40	100.0	451	4	US-09-457-046B-69
19	40	100.0	455	4	US-09-457-046B-72
20	40	100.0	460	4	US-09-457-046B-71
21	40	100.0	461	4	US-09-457-046B-64
22	37	92.5	482	4	US-09-457-046B-63
23	35	87.5	301	4	US-09-457-046B-6
24	35	87.5	433	4	US-09-457-046B-66
25	35	87.5	439	4	US-09-457-046B-26
26	35	87.5	440	4	US-09-457-046B-26
27	35	87.5	440	4	US-09-457-046B-45

28	35	87.5	441	4	US-09-457-046B-54	Sequence 54, Appl
29	35	87.5	443	4	US-09-457-046B-50	Sequence 50, Appl
30	35	87.5	445	4	US-09-457-046B-52	Sequence 52, Appl
31	35	87.5	445	4	US-09-457-046B-73	Sequence 73, Appl
32	35	87.5	497	4	US-09-457-046B-65	Sequence 65, Appl
33	31	77.5	45	2	US-08-726-306A-51	Sequence 51, Appl
34	31	77.5	923	3	US-08-936-135-6	Sequence 6, Appl
35	30	75.0	33	2	US-08-031-538-49	Sequence 49, Appl
36	35	75.0	33	2	US-08-031-538-54	Sequence 54, Appl
37	30	75.0	259	1	US-07-981-707-10	Sequence 10, Appl
38	30	75.0	259	1	US-07-988-430-10	Sequence 10, Appl
39	30	75.0	259	1	US-08-425-336-10	Sequence 10, Appl
40	30	75.0	259	1	US-08-488-113B-10	Sequence 10, Appl
41	30	75.0	259	1	US-08-477-484B-10	Sequence 10, Appl
42	30	75.0	259	2	US-08-646-360-10	Sequence 10, Appl
43	30	75.0	259	4	US-08-839-765-10	Sequence 10, Appl
44	30	75.0	259	4	US-09-136-389-10	Sequence 10, Appl
45	30	75.0	259	5	PCT-US92-09487-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-457-046B-41
; Sequence 41, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paciflaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457, 046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-457-046B-41

Query Match 100.0%; Score 40; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFGWGK 6
|||||
Db 1 DFGWGK 6
RESULT 2
US-09-457-046B-8
; Sequence 8, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paciflaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457, 046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Taxus cuspidata
US-09-457-046B-8

Query Match 100.0%; Score 40; DB 4; Length 302;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWCK 6
|||||
Db 297 DFGWCK 302

RESULT 3
US-09-457-046B-10
Sequence 10, Application US/09457046B

Patent No. 6287835
GENERAL INFORMATION:

APPLICANT: Croteau, Rodney et al.

TITLE OF INVENTION: Transacylases of the Facilitaxel Biosynthetic Pathway

FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B

CURRENT FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentln Ver. 2.1

SEQ ID NO 10
LENGTH: 302

TYPE: PRT

ORGANISM: Taxus cuspidata
US-09-457-046B-10

Query Match 100.0%; Score 40; DB 4; Length 302;
Best Local Similarity 100.0%; Pred. No. 9.3;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWCK 6
|||||
Db 297 DFGWCK 302

RESULT 4
US-09-457-046B-16
Sequence 16, Application US/09457046B

Patent No. 6287835
GENERAL INFORMATION:

APPLICANT: Croteau, Rodney et al.

TITLE OF INVENTION: Transacylases of the Facilitaxel Biosynthetic Pathway

FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B

CURRENT FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentln Ver. 2.1

SEQ ID NO 16
LENGTH: 302

TYPE: PRT

ORGANISM: Taxus cuspidata
US-09-457-046B-16

Query Match 100.0%; Score 40; DB 4; Length 302;
Best Local Similarity 100.0%; Pred. No. 9.3;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWCK 6
|||||
Db 297 DFGWCK 302

RESULT 5
US-09-457-046B-18
Sequence 18, Application US/09457046B

Patent No. 6287835
GENERAL INFORMATION:

APPLICANT: Croteau, Rodney et al.

TITLE OF INVENTION: Transacylases of the Facilitaxel Biosynthetic Pathway

FILE REFERENCE: 53679

CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentln Ver. 2.1

SEQ ID NO 18
LENGTH: 302

TYPE: PRT

ORGANISM: Taxus cuspidata

FEATURE:

NAME/KEY: VARIANT

LOCATION: 164

OTHER INFORMATION: Any amino acid
US-09-457-046B-18

Query Match 100.0%; Score 40; DB 4; Length 302;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWCK 6
|||||
Db 297 DFGWCK 302

RESULT 6
US-09-457-046B-24
Sequence 24, Application US/09457046B

Patent No. 6287835
GENERAL INFORMATION:

APPLICANT: Croteau, Rodney et al.

TITLE OF INVENTION: Transacylases of the Facilitaxel Biosynthetic Pathway

FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B

CURRENT FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentln Ver. 2.1

SEQ ID NO 24
LENGTH: 302

TYPE: PRT

ORGANISM: Taxus cuspidata
US-09-457-046B-24

Query Match 100.0%; Score 40; DB 4; Length 302;
Best Local Similarity 100.0%; Pred. No. 9.3;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWCK 6
|||||
Db 297 DFGWCK 302

RESULT 7
US-09-457-046B-12
Sequence 12, Application US/09457046B

Patent No. 6287835
GENERAL INFORMATION:

APPLICANT: Croteau, Rodney et al.

TITLE OF INVENTION: Transacylases of the Facilitaxel Biosynthetic Pathway

FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B

CURRENT FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentln Ver. 2.1

SEQ ID NO 12
LENGTH: 303

TYPE: PRT

ORGANISM: Taxus cuspidata
US-09-457-046B-12

Query Match 100.0%; Score 40; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 9.3;


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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFGWCK 6
      |||||
Db 298 DFGWCK 303

RESULT 8
US-09-457-046B-20
; Sequence 20, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Pacilitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Taxus cuspidata
US-09-457-046B-20

Query Match 100.0%; Score 40; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFGWCK 6
      |||||
Db 298 DFGWCK 303

RESULT 9
US-09-457-046B-2
; Sequence 2, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Pacilitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Taxus cuspidata
US-09-457-046B-2

Query Match 100.0%; Score 40; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFGWCK 6
      |||||
Db 301 DFGWCK 306

RESULT 10
US-09-457-046B-4
; Sequence 4, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Pacilitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
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; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
+; SEQ ID NO 4
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Taxus cuspidata
US-09-457-046B-4

Query Match 100.0%; Score 40; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFGWCK 6
      |||||
Db 301 DFGWCK 306

RESULT 11
US-09-457-046B-22
; Sequence 22, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Pacilitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Taxus cuspidata
US-09-457-046B-22

Query Match 100.0%; Score 40; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFGWCK 6
      |||||
Db 301 DFGWCK 306

RESULT 12
US-09-457-046B-14
; Sequence 14, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Pacilitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Taxus cuspidata
US-09-457-046B-14

Query Match 100.0%; Score 40; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFGWCK 6
      |||||
Db 317 DFGWCK 322
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RESULT 13
US-09-457-046B-59
; Sequence 59, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-59

Query Match 100.0%; Score 40; DB 4; Length 331;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWCK 6
|||||
Db 265 DFGWCK 270

RESULT 14
US-09-457-046B-62
; Sequence 62, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-62

Query Match 100.0%; Score 40; DB 4; Length 436;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWCK 6
|||||
Db 372 DFGWCK 377

RESULT 15
US-09-457-046B-68
; Sequence 68, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Catharanthus roseus

US-09-457-046B-68

Query Match 100.0%; Score 40; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWCK 6
|||||
Db 380 DFGWCK 385

Search completed: November 5, 2001, 12:58:09
Job time: 70 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 5, 2001, 12:56:59 ; Search time 12.79 Seconds
(without alignments)
35.735 Million cell updates/sec

Title: US-08-894-356c-21

Perfect score: 40

Sequence: 1 DFGWGK 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR6:
2: PIR1:
3: PIR2:
4: PIR3:
5: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	436	2	D86378
2	40	100.0	443	2	T45574
3	40	100.0	450	2	T45573
4	40	100.0	451	2	T00527
5	40	100.0	455	2	T09666
6	40	100.0	460	2	T03274
7	40	100.0	461	2	T00918
8	40	100.0	475	2	T45961
9	37	92.5	399	2	F83484
10	37	92.5	482	2	G84823
11	36	90.0	430	2	T46216
12	35	87.5	439	2	T52321
13	35	87.5	440	2	T52320
14	35	87.5	442	2	T10718
15	35	87.5	445	2	T10717
16	35	87.5	445	2	T10719
17	35	87.5	446	2	T10711
18	35	87.5	464	2	G86453
19	35	87.5	476	2	D84505
20	35	87.5	480	2	H86411
21	35	87.5	485	2	T33865
22	35	87.5	572	2	T01056
23	34	85.0	113	2	S30518
24	34	85.0	129	2	S60978
25	34	85.0	216	2	C85327
26	34	85.0	216	2	T02913
27	34	85.0	303	2	B83336
28	34	85.0	493	2	G84594
29	34	85.0	519	2	S54300

30	34	85.0	667	2	G69723	transketolase (EC
31	34	85.0	741	2	G84888	probable transkeo
32	34	85.0	754	2	T47886	transketolase-like
33	33	82.5	730	2	A75485	hypothetical prote
34	32	80.0	234	2	T36342	response regulator
35	32	80.0	281	2	A86742	hypothetical prote
36	32	80.0	299	2	I36787	hypothetical prote
37	32	80.0	346	2	T10173	24-sterol C-methyl
38	32	80.0	367	2	T06780	probable 24-sterol
39	32	80.0	409	2	T19688	hypothetical prote
40	32	80.0	428	2	T48008	hypothetical prote
41	31	77.5	106	2	B64350	hypothetical prote
42	31	77.5	110	1	F71129	hypothetical prote
43	31	77.5	110	2	F75034	hypothetical prote
44	31	77.5	112	2	J00151	biphenyl-2,3-diol
45	31	77.5	127	2	D82621	hypothetical prote

ALIGNMENTS

RESULT 1
D86378
Protein F21J9.8 [Imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D86378
R:Phenology: A.: Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, R.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo Rizzo, M.; Salzman, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: D86378
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-436 <STO>
A:Cross-references: GB:AE005172; NID:g9743331; PIDN:AAF97955.1; GSPDB:GN00141
C:Genetics:
A:Gene: F21J9.8
A:Map position: 1

Query Match 100.0% Score 40; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGWGK 6
DB 372 DFGWGK 377

RESULT 2
T45574
anthranilate N-hydroxycinnamoyl/phenyltransferase-like protein - Arabidopsis thaliana
N:Alternate names: protein F11C1.120
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C:Accession: T45574
K:Barques, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23007
A:Accession: T45574
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-443 <BAR>
A:Cross-references: EMBL:AL132976
A:Experimental source: Cultivar Columbia; BAC clone F11C1

C:Genetics:
A:Map position: 3
A>Note: F11C1.120

Query Match 100.0%: Score 40; DB 2; Length 443;
Best Local Similarity 100.0%: Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFGWCK 6
|||||
DB 386 DFGWCK 391

RESULT 3
T45573
anthranilate N-hydroxycinnamoyl/benzoyltransferase-like protein - Arabidopsis thaliana
N:Alternate names: protein F11C1.110
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C:Accession: T45573
R:Barques, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May
submitted to the Protein Sequence Database, December 1999
A:Reference number: 223007
A:Accession: T45573
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-450 <BAR>
A:Cross-references: EMBL:AL132976
A:Experimental source: cultivar Columbia; BAC clone F11C1
C:Genetics:
A:Map position: 3
A>Note: F11C1.110

Query Match 100.0%: Score 40; DB 2; Length 450;
Best Local Similarity 100.0%: Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFGWCK 6
|||||
DB 391 DFGWCK 396

RESULT 4
T00527
hypotheetical protein At2g19070 [imported] - Arabidopsis thaliana
N:Alternate names: hypotheetical protein T20K24.8
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 02-Feb-2001
C:Accession: T00527; B84572
R:Rounsley, S.D.; Kaul, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, July 1997
A:Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.
A:Reference number: Z14167
A:Accession: T00527
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-451 <ROD>
A:Cross-references: EMBL:AC002392; NID:g3176701; PID:g3176709
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, X.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKen, S.E.; Umayam, L.; Tallon, L.;
Euss, D.; Nierman, W.C.; White, O.; Eilsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: B84572
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-451 <STO>
A:Cross-references: GB:AB002093; NID:g3176709; PIDN:AAD12025.1; GSPDB:GND0139
C:Genetics:

A:Gene: At2g19070; T20K24.8
A:Map position: 2
A:Introns: 322/1

Query Match 100.0%: Score 40; DB 2; Length 451;
Best Local Similarity 100.0%: Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFGWCK 6
|||||
DB 397 DFGWCK 402

RESULT 5
T09666
probable anthranilate N-benzoyltransferase (EC 2.3.1.144) - muskmelon (fragment)
N:Alternate names: anthranilate N-hydroxycinnamoyl/benzoyltransferase
C:Species: Cucumis melo (muskmelon)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T09666
R:Aggall, A.; John, I.; Karvouni, Z.; Grierson, D.
Plant Mol. Biol. 33, 313-322, 1997
A>Title: Characterization of two cDNA clones for mRNAs expressed during ripening of m
A:Reference number: Z16810; MUID:971188564
A:Accession: T09666
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-455 <AGG>
A:Cross-references: EMBL:Z70521; NID:g1843439; PIDN:CAA94432.1; PID:g1843440
A:Experimental source: cultivar Cantaloupe charentais; pericarp of ripe fruit
C:Keywords: acyltransferase; coenzyme A

Query Match 100.0%: Score 40; DB 2; Length 455;
Best Local Similarity 100.0%: Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFGWCK 6
|||||
DB 374 DFGWCK 379

RESULT 6
T03274
hsr201 protein, hypersensitivity-related - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C:Accession: T03274
R:Czernik, P.; Huang, H.C.; Marco, Y.
Plant Mol. Biol. 31, 255-265, 1996
A>Title: Characterization of hsr201 and hsr515, two tobacco genes preferentially expr
A:Reference number: Z14876; MUID:96343929
A:Accession: T03274
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-460 <CZE>
A:Cross-references: EMBL:X95343; NID:g1171576; PIDN:CAA64636.1; PID:g1171577
A:Experimental source: cultivar bottom special
C:Genetics:
A:Gene: hsr201

Query Match 100.0%: Score 40; DB 2; Length 460;
Best Local Similarity 100.0%: Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFGWCK 6
|||||
DB 382 DFGWCK 387

RESULT 7

T00918
 hypothetical protein F21B7.32 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999
 C:Accession: T00918
 R:Shim, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Cor
 eologs, A.; Ecker, J.R.
 submitted to the EMBL Data Library, January 1998
 A:Description: Genomic sequence for Arabidopsis thaliana BAC F21B7.
 A:Reference number: Z14208
 A:Accession: T00918
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-461 <SH1>
 A:Cross-references: EMBL:AC002560; NID:92618677; PID:92809263; GSPDB:GN00059; ATSP:F21B7
 C:Genetics:
 A:Gene: ATSP:F21B7.32
 A:Map position: 1

Query Match 100.0%; Score 40; DB 2; Length 461;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWK 6
 |||||
 Db 400 DFGWK 405

RESULT 8
 T45961
 anthranilate N-benzoyltransferase-like protein - Arabidopsis thaliana
 N:Alternate names: protein F7J8.190
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
 C:Accession: T45961
 R:Bevan, M.; Zimmermann, W.; Gruenisen, A.; Mambutt, R.; Bancroft, I.; Mewes, H.W.; Lem
 submitted to the Protein Sequence Database, January 2000
 A:Reference number: Z23018
 A:Accession: T45961
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-475 <REV>
 A:Cross-references: EMBL:AL137189
 A:Experimental source: cultivar Columbia; BAC clone F7J8
 C:Genetics:
 A:Map position: 5
 A:Note: F7J8.190

Query Match 100.0%; Score 40; DB 2; Length 475;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWK 6
 |||||
 Db 411 DFGWK 416

RESULT 9
 F83484
 Probable MFS transporter PA1286 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: F83484
 R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
 adman, S.; Vran, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapid, K.; Lim,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950; MUID:20437337
 A:Accession: F83484
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-399 <STO>
 A:Cross-references: GB:AE004558; GB:AE004091; NID:99947217; PIDN:AA04675.1; GSPDB:GN
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA1286

Query Match 92.5%; Score 37; DB 2; Length 399;
 Best Local Similarity 83.3%; Pred. No. 32;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWK 6
 |||||
 Db 36 DFGWK 41

RESULT 10
 G84823
 Probable anthocyanin 5-aromatic acyltransferase [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: G84823
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487
 A:Accession: G84823
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-482 <STO>
 A:Cross-references: GB:AE002093; NID:9208651; PIDN:AAB95283.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g39980
 A:Map position: 2

Query Match 92.5%; Score 37; DB 2; Length 482;
 Best Local Similarity 83.3%; Pred. No. 38;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWK 6
 |||||
 Db 422 DFGWK 427

RESULT 11
 T46216
 hypothetical protein T8P19.230 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 17-Mar-2000
 C:Accession: T46216
 R:Choisne, N.; Robert, C.; Brotlier, P.; Wincker, P.; Cattivello, L.; Artiguenave, F.;
 submitted to the Protein Sequence Database, December 1999
 A:Reference number: Z23008
 A:Accession: T46216
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-430 <CHO>
 A:Cross-references: EMBL:AL133315
 A:Experimental source: cultivar Columbia; BAC clone T8P19
 C:Genetics:
 A:Map position: 3
 A:Introns: 144/3
 A:Note: T8P19.230
 C:Superfamily: Arabidopsis CER2 protein

Query Match 90.0%; Score 36; DB 2; Length 430;
 Best Local Similarity 83.3%; Pred. No. 51;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGWG 6
|||||
Db 378 DFGWG 383

RESULT 12

T52321
taxadienol acetyl transferase [imported] - Taxus cuspidata
C:Species: Taxus cuspidata
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C:Accession: T52321
R:Walker, K.; Schoendorf, A.; Croteau, R.
Submitted to the EMBL Data Library, September 1999
A:Description: Molecular Cloning of a Taxa-4(20),11(12)-dien-5(alpha)-ol-O-Acetyl Transf
A:Reference number: 226036
A:Accession: T52321
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-439 <MAL>
A:Cross-references: EMBL:AF190130; PIDN:AAF34254.1
C:Genetics:
A:Gene: TAT

Query Match 87.5%; Score 35; DB 2; Length 439;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGWG 5
|||||
Db 373 DFGWG 377

RESULT 13

T52320
10-deacetyl baccatin III-10-0-acetyl transferase [imported] - Taxus cuspidata
C:Species: Taxus cuspidata
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C:Accession: T52320
R:Walker, K.; Croteau, R.
Proc. Natl. Acad. Sci. U.S.A. 97, 583-587, 2000
A:Title: Molecular cloning of a 10-deacetyl baccatin III-10-0-acetyl transferase cDNA fr
A:Reference number: 226035
A:Accession: T52320
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-440 <MAL>
A:Cross-references: EMBL:AF193765; PIDN:AAF27621.1
C:Genetics:
A:Gene: DBAT

Query Match 87.5%; Score 35; DB 2; Length 440;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGWG 5
|||||
Db 372 DFGWG 376

RESULT 14

T10718
anthranilate N-benzoyltransferase (EC 2.3.1.144) (clone pchcbt1a) - clove pink (fragment
N:Alternate names: anthranilate N-hydroxycinnamoyl/benzoyltransferase
C:Species: Dianthus caryophyllus (clove pink)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T10718
R:Yang, Q.; Reinhard, K.; Schiltz, E.; Matern, U.
Plant Mol. Biol. 35, 777-789, 1997
A:Title: Characterization and heterologous expression of hydroxycinnamoyl/ benzoyl-CoA:
lus L.

A:Reference number: 217095; MUID:98088004
A:Accession: T10718
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-442 <YAN>
A:Cross-references: EMBL:Z84384; NID:g2239084; PIDN:CAB06428.1; PID:g2239085
C:Function:
A:Description: catalyzes the synthesis of anthranilate
A:Pathway: phytoalexin biosynthesis
C:Keywords: acyltransferase; coenzyme A

Query Match 87.5%; Score 35; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGWG 5
|||||
Db 389 DFGWG 393

RESULT 15

T10717
anthranilate N-benzoyltransferase (EC 2.3.1.144) (clone pchcbt1) - clove pink
N:Alternate names: anthranilate N-hydroxycinnamoyl/benzoyltransferase
C:Species: Dianthus caryophyllus (clove pink)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T10717
R:Yang, Q.; Reinhard, K.; Schiltz, E.; Matern, U.
Plant Mol. Biol. 35, 777-789, 1997
A:Title: Characterization and heterologous expression of hydroxycinnamoyl/ benzoyl-Co
lus L.
A:Reference number: 217095; MUID:98088004
A:Accession: T10717
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-445 <YAN>
A:Cross-references: EMBL:Z84383; NID:g2239082; PIDN:CAB06427.1; PID:g2239083
C:Function:
A:Description: catalyzes the synthesis of anthranilate
A:Pathway: phytoalexin biosynthesis
C:Keywords: acyltransferase; coenzyme A

Query Match 87.5%; Score 35; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGWG 5
|||||
Db 392 DFGWG 396

Search completed: November 5, 2001, 12:57:51
Job time: 52 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 5, 2001, 12:56:59 ; Search: time 10.15 Seconds

(without alignments)
21.674 Million cell updates/sec

Title: US-08-894-356c-21

Perfect score: 40

Sequence: 1 DFGWGK 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	87.5	918	1	HKX1_BOVIN
2	35	87.5	1045	1	Y052_HUMAN
3	34	85.0	129	1	YNO9_YEAST
4	34	85.0	361	1	GP52_HUMAN
5	34	85.0	519	1	TKTC_CRAPL
6	34	85.0	667	1	TKTC_BACSU
7	32	80.0	298	1	VG17_HSV1
8	31	77.5	106	1	Y402_METJA
9	31	77.5	215	1	Y473_AQUAE
10	31	77.5	218	1	FGFF_MOUSE
11	31	77.5	273	1	OPSR_CANFA
12	31	77.5	291	1	BHC1_RHOGO
13	31	77.5	292	1	BPHC_PSESI
14	31	77.5	299	1	BPHC_PSEPA
15	31	77.5	393	1	HEMX_ECOLI
16	31	77.5	484	1	GLGA_BACSU
17	31	77.5	747	1	MEPA_MOUSE
18	31	77.5	748	1	MEPA_MOUSE
19	31	77.5	922	1	MRP1_RAT
20	31	77.5	923	1	MRP1_HUMAN
21	31	77.5	923	1	MRP1_MOUSE
22	31	77.5	1045	1	PRTS_SERMA
23	31	77.5	1045	1	PRTS_SERMA
24	30	75.0	236	1	RIP3_SAPOR
25	30	75.0	253	1	RIP5_SAPOR
26	30	75.0	253	1	RIP7_SAPOR
27	30	75.0	292	1	RIP2_SAPOR
28	30	75.0	293	1	RIP0_DIACA
29	30	75.0	299	1	RIP6_SAPOR
30	30	75.0	357	1	5H5A_HUMAN
31	30	75.0	357	1	5H5A_MOUSE
32	30	75.0	357	1	5H5A_MOUSE
33	30	75.0	370	1	5H5B_MOUSE

34	30	75.0	370	1	5H5B_RAT	P3565_ratus norv
35	30	75.0	420	1	NAP1_HUMAN	O96009 homo sapien
36	30	75.0	451	1	NTF1_ENTHR	P43440 entrococcu
37	30	75.0	474	1	ASCB_ECOLI	P24420 escherichia
38	30	75.0	494	1	CPA8_MESAU	P24454 mesocricetu
39	30	75.0	534	1	YX22_CAEEL	O11193 caenorhabdi
40	30	75.0	618	1	SPPA_ECOLI	P08395 escherichia
41	30	75.0	700	1	YDHY_ECOLI	P76192 escherichia
42	30	75.0	962	1	AMPN_PIG	P15145 sus scrofa
43	30	75.0	1041	1	CHS1_CRYNE	O13356 cryptococcu
44	30	75.0	1213	1	CHS3_CANAL	P30573 candida alb
45	30	75.0	1877	1	PKC5_RAT	P41413 ratus norv

ALIGNMENTS

```

RESULT 1
ID      HKX1_BOVIN      STANDARD;      PRT;      918 AA.
AC      P27595;
DT      01-AUG-1992 (Rel. 23, Created)
DT      01-AUG-1992 (Rel. 23, Last sequence update)
DT      20-AUG-2001 (Rel. 40, Last annotation update)
DE      HEXOKINASE, TYPE I (EC 2.7.1.1) (HK I) (BRAIN FORM HEXOKINASE).
GN      HK1.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=89247146; PubMed=2719857;
RA      Griffin L.D., Macgregor G.R., Muzny D.M., Harter J., Cook R.G.,
RA      McCabe E.R.;
RT      "Synthesis and characterization of a bovine hexokinase 1 cDNA probe
RT      by mixed oligonucleotide primed amplification of cDNA using high
RT      complexity primer mixtures."
RL      Biochem. Med. Metab. Biol. 41:125-131(1989).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=92147056; PubMed=1783373;
RA      Griffin L.D., Gelb B.D., Wheeler D.A., Davison D., Adams V.,
RA      McCabe E.R.;
RT      "Mammalian hexokinase 1: evolutionary conservation and structure to
RT      function analysis."
RL      Genomics 11:1014-1024(1991).
CC      -1- CATALYTIC ACTIVITY: ATP + D-HEXOSE -> ADP + D-HEXOSE 6-PHOSPHATE.
CC      -1- ENZYME REGULATION: HEXOKINASE IS AN ALLOSTERIC ENZYME INHIBITED
CC      BY ITS PRODUCT GLC-6-P.
CC      -1- PATHWAY: FIRST STEP OF SEVERAL METABOLIC PATHWAYS.
CC      -1- SUBUNIT: MONOMER.
CC      -1- SUBCELLULAR LOCATION: BOUND TO THE OUTER MITOCHONDRIAL MEMBRANE.
CC      ITS HYDROPHOBIC N-TERMINAL SEQUENCE MAY BE INVOLVED IN MEMBRANE
CC      BINDING.
CC      -1- MISCELLANEOUS: IN VERTEBRATES THERE ARE FOUR MAJOR GLUCOSE-
CC      PHOSPHORYLATING ISOENZYMES, DESIGNATED HEXOKINASE I, II, III AND
CC      IV (GLUCOKINASE).
CC      -1- SIMILARITY: THE N- AND C-TERMINAL HALVES OF THIS HEXOKINASE
CC      SHOW EXTENSIVE SEQUENCE SIMILARITY TO EACH OTHER. THE CATALYTIC
CC      FUNCTION IS ASSOCIATED WITH THE C-TERMINUS WHILE REGULATORY
CC      ACTIVITY IS ASSOCIATED WITH THE N-TERMINUS.
CC      -1- SIMILARITY: BELONGS TO THE HEXOKINASE FAMILY.
CC      -1- This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      or send an email to license@isb-sib.ch).

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DR EMBL: M65140; AAA51661.1; -
 DR HSPB: P19367; HKB.
 DR InterPro: IPR001312; Hexokinase.
 DR Pfam: PF00349; hexokinase; 2.
 DR PRINTS: PR00475; HEXOKINASE.
 DR ProDom: PD001109; Hexokinase; 2.
 DR PROSITE: PS00378; HEXOKINASES; 2.
 DR Transferrase; Kinase; Glycolysis; Allosteric enzyme; Repeat;
 KW ATP-binding; Membrane.
 FT DOMAIN 1 12 HYDROPHOBIC.
 FT DOMAIN 13 475 REGULATORY (BY SIMILARITY).
 FT DOMAIN 476 918 CATALYTIC (BY SIMILARITY).
 FT DOMAIN 149 175 GLUCOSE-BINDING (POTENTIAL).
 FT DOMAIN 597 623 GLUCOSE-BINDING (POTENTIAL).
 FT NP_BIND 84 89 ATP (POTENTIAL).
 FT NP_BIND 532 537 ATP (POTENTIAL).
 FT BINDING 558 558 ATP (POTENTIAL).
 SQ SEQUENCE 918 AA; 103064 MW; IDCFF7FID06FE2B6 CRC64;

Query Match 87.5%; Score 35; DB 1; Length 918;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWG 5
 |||||
 Db 246 DFGWG 250

RESULT 2
 Y052_HUMAN STANDARD; PRT; 1045 AA.
 AC P42285;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE HYPOTHETICAL PROTEIN KIAA0052 (FRAGMENT).
 GN KIAA0052.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=bone marrow;
 RX MEDLINE=96051398; PubMed=7584044;
 RA Nomura N., Nagase T., Miyajima N., Sazuka T., Sato S.,
 RA Seki N., Kawarabayashi Y., Ishikawa K.-I., Tabata S.;
 RA "Prediction of the coding sequences of unidentified human genes. II.
 RA The coding sequences of 40 new genes (KIAA0041-KIAA0080) deduced by
 RA analysis of cDNA clones from human cell line KG-1.";
 RL DNA Res. 1:223-229(1994).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE SKI2 SUBFAMILY OF HELICASES.
 CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION: A FRAMESHIFT WAS
 CC INTRODUCED IN POSITION 837 TO MAKE THE PROTEIN LONGER AND MAXIMIZE
 CC THE SIMILARITY WITH SKI2.
 CC
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 CC
 CC EMBL: D29641; BAA06124.1; ALT_FRAME.
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR001650; Helicase_C.
 DR Pfam: PF00270; DEAD; 1.
 DR Pfam: PF00271; helicase_C; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HELIC; 1.

KW Hypothetical protein; Helicase; ATP-binding; Nuclear protein.
 FT NON_TER 1 1
 FT NP_BIND 165 172 ATP (POTENTIAL).
 FT SITE 256 259 DEAD BOX.
 SQ SEQUENCE 1045 AA; 118243 MW; 7B16FF8E78049C20 CRC64;

Query Match 87.5%; Score 35; DB 1; Length 1045;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWG 5
 |||||
 Db 672 DFGWG 676

RESULT 3
 YN09_YEAST STANDARD; PRT; 129 AA.
 ID YN09_YEAST
 AC P53903;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE HYPOTHETICAL 15.1 KDA PROTEIN IN RPC8-MEA2 INTERGENIC REGION.
 GN YNL149C OR N1774.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=5288C / FY1679;
 RX MEDLINE=96287653; PubMed=8666380;
 RA Nasr F., Becam A.-M., Herbert C.J.;
 RA "The sequence of 36.8 kb from the left arm of chromosome XIV reveals
 RA 24 complete open reading frames: 18 correspond to new genes, one of
 RA which encodes a protein similar to the human myotonic dystrophy
 RA kinase.";
 RL Yeast 12:169-175(1996).
 RT 12
 RP SEQUENCE OF 1-65 FROM N.A.
 RC STRAIN=5288C;
 RX MEDLINE=96109932; PubMed=8619318;
 RA Waller L., Bussiereau F., Jacquet M.;
 RA "A 43.5 kb segment of yeast chromosome XIV, which contains MEA2,
 RA MEP2, CAP/SRV2, NAM9, FRB1/PPRI/RBP1, MOM22 and CPl1, predicts an
 RA adenosine deaminase gene and 14 new open reading frames.";
 RL Yeast 11:1195-1209(1995).

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 CC
 CC EMBL: X92517; CAA63290.1; -
 DR EMBL: Z71426; CAA96037.1; -
 DR EMBL: Z71424; CAA96033.1; -
 DR SGD: S0005093; YNL149C.
 KW Hypothetical protein.
 SQ SEQUENCE 129 AA; 15053 MW; A1A41E3DA8CEAA06 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 129;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DFGWG 6
 |||||
 Db 84 DFGWG 88

RESULT 4
 GP52_HUMAN STANDARD: PRT; 361 AA.
 AC 09Y275; 075654;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROBABLE G PROTEIN-COUPLED RECEPTOR GPR52.
 GN GPR52.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;
 RX MEDLINE-99132385; PubMed-9911487;
 RA Sawadogo M., Nguyen T., Lee D.K., Lynch K.R., Cheng R., Heng H.H.O.,
 RA George S.R., O'Dowd B.F.;
 RT *Identification and cloning of three novel human G protein-coupled
 RT receptor genes GPR52, PslGPR53 and GPR55: GPR55 is extensively
 RT expressed in human brain.";
 RL Brain Res. Mol. Brain Res. 64:193-198(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Wilkinson J.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ORPHAN RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: AF096784; AAD22409.1; -
 CC EMBL: AL022171; CAA18160.1; -
 CC MIM: 604106; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_FL1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECPT_FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 44
 FT TRANSMEM 45 65
 FT DOMAIN 66 87
 FT TRANSMEM 88 108
 FT DOMAIN 109 116
 FT TRANSMEM 117 137
 FT DOMAIN 138 159
 FT TRANSMEM 160 180
 FT DOMAIN 181 203
 FT TRANSMEM 204 224
 FT DOMAIN 225 265
 FT TRANSMEM 266 286
 FT DOMAIN 287 296
 FT TRANSMEM 297 317
 FT DOMAIN 318 361
 FT CARBOHYD 2 2
 FT CARBOHYD 13 13
 FT CARBOHYD 20 20
 FT CONFLICT 21 21
 FT CONFLICT 64 64
 FT CONFLICT 115 115
 FT CONFLICT 307 307
 FT CONFLICT 322 322
 FT CONFLICT 332 332
 FT CONFLICT 332 332
 FT CONFLICT 332 332
 SO SEQUENCE 361 AA; 41342 MW; C936B47C48F27E6A CRC64;

Query Match 85.0%; Score 34; DB 1; Length 361;
 Best local Similarity 100.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FGWCK 6
 DB 178 FGWCK 182
 RESULT 5
 TRKC_CRAPL STANDARD: PRT; 519 AA.
 ID TRKC_CRAPL
 AC Q42676;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE TRANSKETOLASE, CHLOROPLAST (EC 2.2.1.1) (TK) (FRAGMENT).
 GN TKT3.
 OS Craterostigma plantagineum.
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Lamiales incertae sedis; Toreneae;
 OC Craterostigma.
 NCBI_TaxId=4153;
 RX MEDLINE-95163594; PubMed-7859749;
 RA Bernacchia G., Schwall G., Lottspeich F., Salami F., Bartels D.;
 RT "The transketolase gene family of the resurrection plant
 RT Craterostigma plantagineum: differential expression during the
 RT rehydration phase.";
 RL EMBL J. 14:610-618(1995).
 CC -1- CATALYTIC ACTIVITY: SEDOHEPTULOSE 7-PHOSPHATE + D-GLYCERALDEHYDE
 CC 3-PHOSPHATE -> D-RIBOSE 5-PHOSPHATE + D-XYLULOSE 5-PHOSPHATE.
 CC -1- COFACTOR: THIAMINE PYRROPHOSPHATE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN LEAVES AND ROOTS.
 CC -1- SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: Z46646; CAA86607.1; -
 CC HSSP: P33254; 1TKA.
 DR InterPro: IPR00360; Transketolase.
 DR Pfam: PF00456; transketolase; 1.
 DR PROSITE: PS00801; TRANSKETOLASE_1; PARTIAL.
 DR PROSITE: PS00802; TRANSKETOLASE_2; 1.
 KW Transferrase; Thiamine pyrophosphate; Chloroplast; Multigene family.
 FT NON_TER 1 1
 SO SEQUENCE 519 AA; 56187 MW; 7AFD034CE2BC5685 CRC64;
 Query Match 85.0%; Score 34; DB 1; Length 519;
 Best local Similarity 100.0%; Pred. No. 63;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FGWCK 6
 DB 473 FGWCK 477
 RESULT 6
 TKT_BACSU STANDARD: PRT; 667 AA.
 ID TKT_BACSU

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AC P45694:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE TRANSEKTOLOASE (EC 2.2.1.1).
GN TKT OR TKTa.
OS Bacillus subtilis.
OC Bacteria, Firmicutes, Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OC NCBI_TaxID=1423;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168.
RA Rose M., Entian K.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE OF 561-667 FROM N.A.
RC STRAIN=168.
RA Schott T., von Machenfeldt C., Hederstedt L.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: SEDOHEPTULOSE 7-PHOSPHATE + D-GLYCERALDEHYDE
CC 3-PHOSPHATE -> D-RIBOSE 5-PHOSPHATE + D-XULULOSE 5-PHOSPHATE.
CC -1- COPACTOR: THIAMINE PYROPHOSPHATE.
CC -1- SIMILARITY: BELONGS TO THE TRANSEKTOLOASE FAMILY.
CC -----
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CC -----
DR EMBL: 273234; CAA97616.1; -
DR EMBL: X87845; CAA61113.1; -
DR EMBL: 299113; CAB13673.1; -
DR HSSP: P23254; IAYO
DR Subtilist; BG11247; Tkt.
DR InterPro: IPR000360; Transketolase.
DR Pfam: PF00456; transketolase; 1.
DR PROSITE: PS00801; TRANSEKTOLOASE_1; 1.
DR PROSITE: PS00802; TRANSEKTOLOASE_2; 1.
KW Transferrase: Thiamine pyrophosphate; Complete proteome.
SQ SEQUENCE 667 AA; 72344 MW; D93BCACD246148AF CRC64;

Query Match          85.0%; Score 34; DB 1; Length 667;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FCGWCK 6
DB 619 FCGWCK 623

RESULT 7
VGI7_HSVI1          STANDARD; PRT; 298 AA.
ID VGI7_HSVI1
AC Q00016;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DE 01-DEC-1992 (Rel. 24, Last annotation update)
DE HYPOHETICAL GENE 17 PROTEIN.
GN 17.
OS Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
OC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;
OC unclassified Herpesviridae.
OX NCBI_TaxID=10401;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AUBURN 1;
RX MEDLINE=92087490; PubMed=1727613;
RA Davison A.J.;

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RT "Channel catfish virus: a new type of herpesvirus.";
RL Virology 186:9-14(1992).
CC -----
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CC -----
DR EMBL: M75136; AAA88120.1; -
DR F184; 136787; 136787.
KW Hypothetical protein.
SQ SEQUENCE 298 AA; 32399 MW; 4C90B1DEEA203FA9 CRC64;

Query Match          80.0%; Score 32; DB 1; Length 298;
Best Local Similarity 66.7%; Pred. No. 85;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFCWCK 6
DB 67 DFCWCK 72

RESULT 8
Y402_METJA          STANDARD; PRT; 106 AA.
ID Y402_METJA
AC Q57845;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOHETICAL PROTEIN MJ0402.
GN MJ0402.
OS Methanococcus jannaschii.
OC Archaea, Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bull C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutcliffe G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kierulff A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reisch C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Ullrichbeck T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Klenk H.-P., Fraser C.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RA jannaschii."
RT Science 273:1058-1073(1996).
RL -----
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CC -----
DR EMBL: U67492; AAB98395.1; -
DR TIGR: MJ0402; -
KW Hypothetical protein: Complete proteome.
SQ SEQUENCE 106 AA; 12600 MW; 6398888ABD46CF93 CRC64;

Query Match          77.5%; Score 31; DB 1; Length 106;
Best Local Similarity 80.0%; Pred. No. 52;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 2 FGWCK 6
DB 2 FGWGR 6

RESULT 9
Y473_AOUAE STANDARD: PRT; 215 AA.

AC 066771;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE HYPOTHETICAL PROTEIN AQ_473.

GN AQ_473.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxId=63363;

RP SEQUENCE FROM N.A.
RC STRAIN=VF5;

RX MEDLINE=98196666; PubMed=9537320;

RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Sneed M.A., Anujay M., Huber R.,

RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex

aeolicus";
RT Nature 392:353-358(1998).

CC -1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

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DR EMBL: AF000691; AAC06731.1; -
KW Hypothetical protein; Transmembrane; Complete proteome.

FT TRANSMEM 77 99 POTENTIAL.
FT TRANSMEM 117 139 POTENTIAL.
FT TRANSMEM 152 174 POTENTIAL.
FT TRANSMEM 189 208 POTENTIAL.

FT SEQUENCE 215 AA; 23986 MW; BE87A517459DAECC CRC64;

Query Match 77.5%; Score 31; DB 1; Length 215;
Best Local Similarity 80.0%; Pred. No. 95;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 FGWCK 6
DB 85 YGWCK 89

RESULT 10
FGFF_MOUSE STANDARD: PRT; 218 AA.

AC 035622;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE FIBROBLAST GROWTH FACTOR-15 PRECURSOR (FGF-15).
GN FGF15.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;

RP SEQUENCE FROM N.A.
RN MEDLINE=97454242; PubMed=9310317;

RA McWhirter J.R., Goulding M., Weiner J.A., Chun J., Murre C.;
RT "A novel fibroblast growth factor gene expressed in the developing

RT nervous system is a downstream target of the chimeric homeodomain
RT oncoprotein E2A-Pbx1.";

CC -1 FUNCTION: MAY PLAY AN IMPORTANT ROLE IN REGULATING CELL DIVISION
AND PATTERNING WITHIN SPECIFIC REGIONS OF THE EMBRYONIC BRAIN.

CC -1 SUBCELLULAR LOCATION: SECRETED.
CC -1 TISSUE SPECIFICITY: EXPRESSED IN THE DEVELOPING BRAIN.

CC -1 SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.

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DR EMBL: AF007268; AAB63197.1; -
DR MCD: MGI:1096383; Fgf15.

DR InterPro: IPR002209; HBG_FGF.
DR InterPro: IPR002348; IL1_HBGF.

DR Pfam: PF00167; FGF_1.
DR PRINTS: PR00262; IL1HBGF.

DR PRODOM: PD000831; HBG_FGF; 1.
DR SMART: SM00442; FGF_1.

DR PROSITE: PS00247; HBG_FGF; 1.
KW Growth factor; Signal.

FT CHAIN 1 25 POTENTIAL.
FT SEQUENCE 218 AA; 25236 MW; A96B0D771FE125A5 CRC64;

Query Match 77.5%; Score 31; DB 1; Length 218;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 FGWCK 6
DB 44 YGWCK 48

RESULT 11
OPSR_CANFA STANDARD: PRT; 273 AA.

ID OPSR_CANFA 018914;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE RED-SENSITIVE OPSIN (RED CONE PHOTORECEPTOR PIGMENT) (FRAGMENT).
GN OPN1LM OR RCP.

OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxId=9615;

RP SEQUENCE FROM N.A.
RX MEDLINE=98242086; PubMed=9580985;

RA Yokoyama S., Radlwimmer F.B.;
RT "The 'five-sites' rule and the evolution of red and green color

vision in mammals.";
RL Mol. Biol. Evol. 15:560-567(1998).

CC -1 FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
LINKED TO CIS-RETINAL.

CC -1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1 TISSUE SPECIFICITY: THE THREE COLOR PIGMENTS ARE FOUND IN THE CONE
PHOTORECEPTOR CELLS.

CC -1 PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
BE PHOSPHORYLATED.

CC -1 SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC OPSIN SUBFAMILY.

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CC -----
 CC EMBL: AF031533; AAB86633.1; -
 CC GCRDB: GCR2500; -
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC InterPro: IPR001760; Opsin.
 CC Pfam: PF00001; 7tm_1; 1.
 CC PROSITE: PS00237; G-PROTEIN_RECEPTOR_F1_1; 1.
 CC PROSITE: PS50262; G-PROTEIN_RECEPTOR_F1_2; 1.
 CC PROSITE: PS00238; OPSIN; PARTIAL.
 CC Photoreceptor: Retinal protein: Transmembrane; Glycoprotein; Vision;
 KW phosphorylation; Lipoprotein; Palmitate; G-protein coupled receptor.
 FT NON_TER 1 1
 FT DOMAIN 1 1
 FT TRANSMEM 6 5
 FT DOMAIN 31 30
 FT TRANSMEM 43 42
 FT TRANSMEM 69 68
 FT TRANSMEM 83 82
 FT TRANSMEM 103 102
 FT TRANSMEM 122 121
 FT TRANSMEM 146 145
 FT TRANSMEM 172 171
 FT TRANSMEM 199 198
 FT TRANSMEM 220 219
 FT TRANSMEM 246 245
 FT TRANSMEM 254 253
 FT DISULFID 79 156
 FT BINDING 265 265
 FT NON_TER 273 273
 FT SEQUENCE 273 AA; 30373 MW; C1A27C95D1649F85 CRC64;

Query Match 77.5%; Score 31; DB 1; Length 273;
 Best Local Similarity 80.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 FEGWK 6
 DB 142 FEGWK 146

RESULT 12
 BHCL_RHGO STANDARD; PRT; 291 AA.
 ID BHCL_RHGO
 AC P47231;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE BIHENTYL-2,3-DIOL 1,2-DIOXYGENASE I (EC 1.13.11.39) (230HP
 DE OXYGENASE I) (2,3-DIHYDROXYBIHENTYL DIOXYGENASE I) (DHBD I).
 GN BPHC1.
 OS Rhodococcus globerulus.
 CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Corynebacteriaceae; Nocardiaceae; Rhodococcus.
 CC NCB1_TaxID=33008;
 OX NCB1
 RN NCB1
 RP SEQUENCE FROM N.A.
 RC STRAIN=P6;
 RX MEDLINE=94171820; PubMed=8126007;
 RA Asturias J.A., Ellis L.D., Prucha M., Timmis K.N.,
 RT "Analysis of three 2,3-dihydroxybiphenyl 1,2-dioxygenases found in
 RT Rhodococcus globerulus P6. Identification of a new family of
 RT extradiol dioxygenases.";
 RL J. Biol. Chem. 269:7807-7815(1994).
 CC -1- CATALYTIC ACTIVITY: BIHENTYL-2,3-DIOL + O(2) = 2-HYDROXY-6-OXO-
 CC 6-PHENYLHEXA-2,4-DIENATE + H(2)O.

CC -1- COFACTOR: FERROUS ION.
 CC -1- PATHWAY: DEGRADATION OF BIHENTYLS AND POLYCHLOROBIPHENYLS (PCB) TO
 CC BENZOIC ACID AND CHLOROBENZOIC ACIDS.
 CC -1- SIMILARITY: BELONGS TO THE EXTRADIOL RING-CLEAVAGE DIOXYGENASE
 CC FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL: X75633; CA53297.1; -
 CC HSSP: P47228; 1HAN.
 CC InterPro: IPR000486; Extradiol_dioxygenase.
 CC InterPro: IPR000325; Glyoxalase_1.
 CC Pfam: PF00903; Glyoxalase; 1.
 CC ProDom: PD000977; Extradiol_dioxygenase; 1.
 CC PROSITE: PS00082; EXTRADIOL_DIOXYGENAS; 1.
 CC Oxidoreductase: Dioxygenase: Aromatic hydrocarbons catabolism; Iron.
 FT METAL 146 146
 FT METAL 210 210
 FT METAL 260 260
 FT SEQUENCE 291 AA; 32081 MW; 104F189FE1EDDA6A CRC64;

Query Match 77.5%; Score 31; DB 1; Length 291;
 Best Local Similarity 80.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DEFGW 5
 DB 260 DEFGW 264

RESULT 13
 BPHC_PSES1 STANDARD; PRT; 292 AA.
 ID BPHC_PSES1
 AC P17297; 052441;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE BIHENTYL-2,3-DIOL 1,2-DIOXYGENASE (EC 1.13.11.39) (230HP OXYGENASE)
 DE (2,3-DIHYDROXYBIHENTYL DIOXYGENASE) (DHBD).
 GN BPHC.
 OS Pseudomonas sp. (strain KKS102).
 CC Bacteria; Proteobacteria.
 CC NCB1_TaxID=307;
 OX NCB1
 RN NCB1
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89213965; PubMed=2540155;
 RA Kimbara K., Hashimoto T., Fukuda M., Koana T., Takagi M., Oishi M.,
 RT Yano K.;
 RT "Cloning and sequencing of two tandem genes involved in degradation
 RT of 2,3-dihydroxybiphenyl to benzoic acid in the polychlorinated
 RT biphenyl-degrading soil bacterium Pseudomonas sp. strain KKS102.";
 RL J. Bacteriol. 171:2740-2747(1989).
 CC [2]
 CC X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 CC MEDLINE=96226036; PubMed=8636975;
 RA Senda T., Sugiyama K., Narita H., Yamamoto T., Kimbara K., Fukuda M.,
 RA Sato M., Yano K., Mitsui Y.;
 RT "Three-dimensional structures of free form and two substrate
 RT complexes of an extradiol ring-cleavage type dioxygenase, the BphC
 RT enzyme from Pseudomonas sp. strain KKS102.";
 RL J. Mol. Biol. 255:735-752(1996).
 CC -1- CATALYTIC ACTIVITY: BIHENTYL-2,3-DIOL + O(2) = 2-HYDROXY-6-OXO-
 CC 6-PHENYLHEXA-2,4-DIENATE + H(2)O.
 CC -1- COFACTOR: FERROUS ION.
 CC -1- PATHWAY: DEGRADATION OF BIHENTYLS AND POLYCHLOROBIPHENYLS (PCB) TO
 CC BENZOIC ACID AND CHLOROBENZOIC ACIDS.

CC -1- SUBUNIT: HOMOOCTAMER.
CC -1- SIMILARITY: BELONGS TO THE EXTRADIOL RING-CLEAVAGE DIOXYGENASE
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M26443; AAA25750.1; -
CC EMBL: D17319; BAA04141.1; -
CC PIR: A32312; DAPSPC.
CC PDB: 1DHY; 15-OCT-95.
CC InterPro: IPR000486; Extradiol_dioxygenase.
CC InterPro: IPR000325; Glyoxalase_1.
CC Pfam: PF00903; Glyoxalase; 2.
CC ProDom: PD000977; Extradiol_dioxygenase; 1.
CC PROSITE: PS00082; EXTRADIOL_DIOXYGENAS; 1.
CC Oxidoreductase; Dioxigenase; Aromatic hydrocarbons catabolism; Iron;
KM 3D-structure.
FT INIT_MER 0 0
FT METAL 145 145 IRON.
FT METAL 209 209 IRON.
FT METAL 260 260 IRON.
SQ SEQUENCE 292 AA; 32113 MW; 5D7D912F79EA8476 CRC64;

Query Match 77.5%; Score 31; DB 1; Length 292;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWG 5
:||||
Db 260 EFGWG 264

RESULT 14
BPHC_PSEPA
ID BPHC_PSEPA STANDARD; PRT; 299 AA.
AC P11122;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE BIPIENYL-2,3-DIOL 1,2-DIOXYGENASE (EC 1.13.11.39) (23OHP OXYGENASE)
DE (2,3-DIHYDROXYBIPIENYL DIOXYGENASE) (OHPD).
GN BPHC.
OS Pseudomonas paucimobilis (Sphingomonas paucimobilis).
OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
OC Sphingomonas.
OX NCBI_TaxID=13689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Q1;
RX MEDLINE=88326911; PubMed=3137968;
RA Taira K., Hayase N., Arimura N., Yamashita S., Miyazaki T.,
RA Furukawa K.;
RT Cloning and nucleotide sequence of the 2,3-dihydroxybiphenyl
dioxygenase gene from the PCB-degrading strain of Pseudomonas
paucimobilis O1.";
RL Biochemistry 27:3990-3996(1988).
CC -1- CATALYTIC ACTIVITY: BIPIENYL-2,3-DIOL + O(2) - 2-HYDROXY-6-EXO-
CC 6-PHENYLHEXA-2,4-DIENATE + H(2)O.
CC -1- COFACTOR: FERROUS ION.
CC -1- PATHWAY: DEGRADATION OF BIPIENYLS AND POLYCHLOROBIPHENYLS (PCB) TO
CC BENZOIC ACID AND CHLOROBENZOIC ACIDS.
CC -1- SUBUNIT: HOMOOCTAMER.
CC -1- SIMILARITY: BELONGS TO THE EXTRADIOL RING-CLEAVAGE DIOXYGENASE
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M20640; AAA25678.1; -
CC PIR: A28718; A28718.
CC HSSP: P17297; 1DHY.
CC InterPro: IPR000486; Extradiol_dioxygenase.
CC InterPro: IPR000325; Glyoxalase_1.
CC Pfam: PF00903; Glyoxalase; 2.
CC ProDom: PD000977; Extradiol_dioxygenase; 1.
CC PROSITE: PS00082; EXTRADIOL_DIOXYGENAS; 1.
CC Oxidoreductase; Dioxigenase; Aromatic hydrocarbons catabolism; Iron.
KM METAL 149 149 IRON (BY SIMILARITY).
FT METAL 212 212 IRON (BY SIMILARITY).
FT METAL 263 263 IRON (BY SIMILARITY).
SQ SEQUENCE 299 AA; 33095 MW; 29746CAB79D6FC7B CRC64;

Query Match 77.5%; Score 31; DB 1; Length 299;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWG 5
:||||
Db 263 EFGWG 267

RESULT 15
HEMX_ECOLI
ID HEMX_ECOLI STANDARD; PRT; 393 AA.
AC P09127;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PUTATIVE UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) (UROGEN
DE III METHYLASE) (ORF X).
GN HEMX OR B3803.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=89098348; PubMed=3062586;
RA Sasarman A., Echeland Y., Letowski J., Tardif D., Drolet M.,
RT "Nucleotide sequence of the hemX gene, the third member of the uro
RT operon of Escherichia coli K12";
RL Nucleic Acids Res. 16:11835-11835(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / CS520;
RX MEDLINE=89041586; PubMed=3054815;
RA Alefounder P.R.;
RT "The sequence of hemC, hemD and two additional E. coli genes";
RL Nucleic Acids Res. 16:9871-9871(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=92358234; PubMed=1379743;
RA Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
RT "Analysis of the Escherichia coli genome: DNA sequence of the region
RL from 84.5 to 86.5 minutes.";
RL Science 257:771-778(1992).
RN [4]
RP SEQUENCE OF 1-12.
RC STRAIN-K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.D., Robison K., Church G.M.;

```
RT      "Comparing the predicted and observed properties of proteins encoded
RL      in the genome of Escherichia coli K-12."
CC      Electrophoresis 18:1259-1313(1997).
CC      -1- CATALYTIC ACTIVITY: 2 S-ADENOSYL-L-METHIONINE + UROPORPHYRIN III
CC      = 2 S-ADENOSYL-L-HOMOCYSTEINE + SIROHYDROCHLORIN.
CC      -1- PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF SIROHEME AND COBALAMIN.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X13406; CAA31772.1; -
DR      EMBL; X12614; CAA31134.1; -
DR      EMBL; M87049; AAA67599.1; -
DR      EMBL; AE000456; AAC76806.1; -
DR      PIR; S02185; S02185.
DR      PIR; S30693; S30693.
DR      ECO2DBASE; B043.0; 6TH EDITION.
DR      ECO2DBASE; B043.1; 6TH EDITION.
DR      EcoGene; EG10433; hemX.
KW      Porphyrin biosynthesis; Transferase; Methyltransferase;
KW      Complete proteome.
SQ      SEQUENCE 393 AA; 42963 MW; 9D272C6401D0E354 CRC64;
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Query Match          77.5%; Score 31; DB 1; Length 393;
Best Local Similarity 80.0%; Pred No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Oy      2 FGVGK 6
       :||||
DB      55 YGVGK 59
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Search completed: November 5, 2001, 12:58:55
Job time: 116 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 5, 2001, 12:56:59 ; Search time 22.88 Seconds
(without alignments)
38.358 Million cell updates/sec

Title: US-08-894-356C-21
Perfect score: 40
Sequence: 1 DFGWGK 6

Scoring table:
BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP-archaea:.*
2: SP-bacteria:.*
3: SP-fungi:.*
4: SP-human:.*
5: SP-invertebrate:.*
6: SP-mammal:.*
7: SP-mhc:.*
8: SP-organella:.*
9: SP-phage:.*
10: SP-plant:.*
11: SP-rodent:.*
12: SP-virus:.*
13: SP-vertebrate:.*
14: SP-unclassified:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	219	10	Q9M5K9 euphorbia e
2	40	100.0	434	10	Q9FH97 arabidopsis
3	40	100.0	435	10	Q9PYM0 arabidopsis
4	40	100.0	436	10	Q9PYM1 arabidopsis
5	40	100.0	439	10	Q9ZTK5 arabidopsis
6	40	100.0	442	10	Q9FFA3 arabidopsis
7	40	100.0	443	10	Q9SND9 arabidopsis
8	40	100.0	443	10	Q9FJNO arabidopsis
9	40	100.0	446	10	Q9MBC1 arabidopsis
10	40	100.0	448	10	Q9MBD4 arabidopsis
11	40	100.0	448	10	Q9FID1 arabidopsis
12	40	100.0	448	10	Q9FH98 arabidopsis
13	40	100.0	449	10	Q9LJH4 arabidopsis
14	40	100.0	450	10	Q9SNE0 arabidopsis
15	40	100.0	451	10	Q9M470 arabidopsis
16	40	100.0	455	10	P93094 cucumis mel
17	40	100.0	455	10	Q9LU88 arabidopsis
18	40	100.0	458	10	Q9LJA2 arabidopsis
19	40	100.0	460	10	Q43583 nicotiana t

20	40	100.0	461	10	Q9LR83 arabidopsis
21	40	100.0	469	10	Q9ZWR8 gentiana tr
22	40	100.0	475	10	Q9LFB5 arabidopsis
23	40	100.0	479	10	Q9MBD5 gentiana tr
24	40	100.0	553	10	Q9FVY9 oryza sativ
25	37	92.5	99	10	Q23943 fragaria ve
26	37	92.5	180	10	Q9LR06 arabidopsis
27	37	92.5	293	10	Q9FSP0 oryza sativ
28	37	92.5	399	2	Q91458 pseudomonas
29	37	92.5	431	10	Q9SST8 ipomoea bat
30	37	92.5	433	10	Q9FI78 arabidopsis
31	37	92.5	443	10	Q9FI40 arabidopsis
32	37	92.5	451	10	Q9LR08 arabidopsis
33	37	92.5	451	10	Q9LR07 arabidopsis
34	37	92.5	452	10	Q9FVFI fragaria an
35	37	92.5	452	10	Q9FNP9 arabidopsis
36	37	92.5	455	10	Q9FID3 arabidopsis
37	37	92.5	463	10	Q9FID2 arabidopsis
38	37	92.5	482	10	Q04201 arabidopsis
39	36	90.0	280	10	Q04201 arabidopsis
40	36	90.0	426	10	Q9FVQ7 prunus arme
41	36	90.0	430	10	Q9SMW7 arabidopsis
42	36	90.0	441	10	Q9FLM5 arabidopsis
43	35	87.5	363	2	Q9A0Q7 streptococ
44	35	87.5	428	10	Q9FLW4 arabidopsis
45	35	87.5	430	10	Q9SQ02 clarkia con

ALIGNMENTS

RESULT 1
ID Q9M5K9 PRELIMINARY: PRT: 219 AA.
AC Q9M5K9:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE F21J9.20-LIKE PROTEIN (FRAGMENT).
OS Euphorbia esula (leafy spurge).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC eurosids I; Malpighiales; Euphorbiaceae; Euphorbia.
OX NCBI_TaxID=3993;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UNDERGROUND ADVENTITIOUS BUDS;
RA Anderson J.V., Horvath D.P.;
RT "Identification of mRNAs expressed in underground adventitious buds of
RT Euphorbia esula (leafy spurge).";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF227981; AAF34801.1; -
FT NON-TER 1
SQ SEQUENCE 219 AA: 24236 MW: DDD96C93FC87BC30 CRC64;

Query Match 100.0%; Score 40; DB 10; Length 219;
Best local Similarity 100.0%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGWGK 6
DB 155 DFGWGK 161

RESULT 2
ID Q9FH97 PRELIMINARY: PRT: 434 AA.
AC Q9FH97:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ANTHANILATE N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE-LIKE PROTEIN.

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 OK NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20181125; PubMed=10718197;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
 RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
 RT clones";
 RL DNA Res. 7:31-63(2000).
 DR EMBL; AB020742; BAB10950.1; -
 DR InterPro: IPR003480; Transferase.
 DR Pfam: PF02458; Transferase; 1.
 KW Transferase
 SO SEQUENCE 434 AA; 48635 MW; 7E4C4C61DA1624AA CRC64;

Query Match 100.0%; Score 40; DB 10; Length 434;

Best Local Similarity 100.0%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DEGCK 6

DB 376 DEGWCK 381

RESULT 3

O9FYMO PRELIMINARY; PRT; 435 AA.
 AC O9FYMO:
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE F21J9.9.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 OK NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C.,
 RA Shinn P., Altafi H., Bel O., Chin C., Chlou J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howling B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharzky N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thayerl A.,
 RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
 RA Ecker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC F21J9 from chromosome
 RT 1";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.

RA Ecker J.R.;

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

RN [7]

RP SEQUENCE FROM N.A.

RA Ecker J.R.;

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

RN [8]

RP SEQUENCE FROM N.A.

RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Altafi H., Bel O., Chin C., Chlou J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howling B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharzky N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Thayerl A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
 RA Theologis A., Ecker J.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [9]

RP SEQUENCE FROM N.A.

RA Ecker J.R.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [10]

RP SEQUENCE FROM N.A.

RA Ecker J.R.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [11]

RP SEQUENCE FROM N.A.

RA Ecker J.R.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [12]

RP SEQUENCE FROM N.A.

RA Ecker J.R.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [13]

RP SEQUENCE FROM N.A.

RA Ecker J.R.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [14]

RP SEQUENCE FROM N.A.

RA Ecker J.R.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [15]

RP SEQUENCE FROM N.A.

RA Ecker J.R.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [16]

RP SEQUENCE FROM N.A.

RA Ecker J.R.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [17]

RP SEQUENCE FROM N.A.

RA Ecker J.R.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [18]

RP SEQUENCE FROM N.A.

RA Ecker J.R.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [19]

RP SEQUENCE FROM N.A.

RA Ecker J.R.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [20]

RP SEQUENCE FROM N.A.

RA Ecker J.R.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [21]

RP SEQUENCE FROM N.A.

RA Ecker J.R.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [22]

RP SEQUENCE FROM N.A.

RA Ecker J.R.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [23]

RP SEQUENCE FROM N.A.

RA Ecker J.R.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [6]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RA Chen R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Altai H., Bel B., Chin C., Chou J., Choi E.,
 RA Com L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukhazsky N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Theverl A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC000103; AAF97955.1; -;
 DR InterPro: IPR003480; Transferase.
 DR Pfam: PF02458; Transferase; 1.
 SO SEQUENCE 436 AA; 48824 MW; B303A52DE3FD1355 CRC64;

Query Match 100.0%; Score 40; DB 10; Length 436;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWGK 6
 Db 372 DFGWGK 377

RESULT 5
 ID 092TK5 PRELIMINARY; PRT; 439 AA.
 AC 092TK5;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE DEACTYLAVINDOLINE 4-O-ACETYLTRANSFERASE (EC 2.3.1.107).
 GN DAT.
 OS Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; eusterids I; Gentianales; Apocynaceae; Catharanthus.
 OX NCBI_TaxID=4058;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV LITTLE DELICATA;
 RX MEDLINE-98346012; PubMed-9681034;
 RA St-Pierre B., Laflamme P., Alarco A.M., De Luca V.;
 RT "The terminal O-acetyltransferase involved in vindoline biosyntheses
 RT defines a new class of proteins responsible for coenzyme A-dependent
 RT acyl transfer.";
 RL Plant J. 14:703-713(1998).
 DR EMBL: AF053307; AAC9311.1; -;
 DR InterPro: IPR003480; Transferase.
 DR Pfam: PF02458; Transferase; 1.
 KW Transferase; Acyltransferase.
 SO SEQUENCE 439 AA; 49873 MW; 1357C76550E0D04D CRC64;

Query Match 100.0%; Score 40; DB 10; Length 439;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWGK 6
 Db 380 DFGWGK 385

RESULT 6

09FF43
 ID 09FF43 PRELIMINARY; PRT; 442 AA.
 AC 09FF43;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE ANTHRANILATE N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE-LIKE PROTEIN.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustoids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RX MEDLINE-97471969; PubMed-9330910;
 RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
 RA Miyajima N., Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
 RT features of the 1.6 Mb regions covered by twenty physically assigned
 RT pl clones.";
 RL DNA Res. 4:215-230(1997).
 DR EMBL: AB005247; BAB11280.1; -;
 DR InterPro: IPR003480; Transferase.
 DR Pfam: PF02458; Transferase; 1.
 KW Transferase.
 SO SEQUENCE 442 AA; 49491 MW; 1D280C885875DA47 CRC64;

Query Match 100.0%; Score 40; DB 10; Length 442;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWGK 6
 Db 384 DFGWGK 389

RESULT 7
 ID 09SND9 PRELIMINARY; PRT; 443 AA.
 AC 09SND9;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE ANTHRANILATE N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE-LIKE PROTEIN.
 GN F1C1.120.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustoids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barques M., Collado M.C., Navarro P., Terol J., Perez-Alonso M.,
 RA Mewes H.W., Lemcke K., Mayer K.F.X., Queller F., Salanoubat M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC EU Arabidopsis sequencing project;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL132976; CAB62307.1; -;
 DR InterPro: IPR003480; Transferase.
 DR Pfam: PF02458; Transferase; 1.
 KW Transferase.
 SO SEQUENCE 443 AA; 49960 MW; C4ADB67A0E3AB3D4 CRC64;

Query Match 100.0%; Score 40; DB 10; Length 443;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWGK 6

Db 386 DFGWK 391

RESULT 8

ID Q9FJNO PRELIMINARY; PRT: 443 AA.

AC Q9FJNO; 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98403884; PubMed=9734815;
RA Kotani H., Nakamura Y., Sato S., Asanizu E., Kaneko T., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RT Sequence features of the regions of 1,367,185 bp covered by 19
RT physically assigned P1 and TAC clones."
RL DNA Res. 5:203-216(1998).
DR EMBL; AB013396; BAB08854.1; -
DR InterPro: IPR003480; Transferase.
DR Pfam: PF02458; Transferase; 1.
KW TRANSFERASE.
SQ SEQUENCE 443 AA; 49950 MW; 16FFC01B99035AD CRC64;

Query Match Best Local Similarity 100.0%; Score 40; DB 10; Length 443;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWK 6
Db 385 DFGWK 390

RESULT 9
ID Q9MBCL PRELIMINARY; PRT: 446 AA.

AC Q9MBCL; 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE ANTHOCYANIN ACYLTRANSFERASE (FRAGMENT).
OS Perilla frutescens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla.
OX NCBI_TaxID=48386;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAF;
RA Sakakibara K.Y., Tanaka Y., Mizutani M.F., Fujiwara H., Fukui Y.,
RA Ashikari T., Yamaguchi M., Kusumi T.;
RT "Molecular and biochemical characterization of a novel
RT hydroxycinnamoyl-CoA: anthocyanin 3-O-glucoside-6-"
RT Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
RL EMBL; AB029340; BAA93475.1; -
DR InterPro: IPR003480; Transferase.
DR Pfam: PF02458; Transferase; 1.
KW TRANSFERASE; Acyltransferase.
FT NON_TER 1
SQ SEQUENCE 446 AA; 50675 MW; DC83C69AF248A593 CRC64;

Query Match 100.0%; Score 40; DB 10; Length 446;

Best Local Similarity 100.0%; Pred. NO. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWK 6
Db 389 DFGWK 394

RESULT 10

ID Q9MBD4 PRELIMINARY; PRT: 448 AA.

AC Q9MBD4; 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE ACYLTRANSFERASE HOMOLOG.
GN PAT48.
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]
RP SEQUENCE FROM N.A.
RA Yonekura-Sakakibara K., Tanaka Y., Fukuchi-Mizutani M., Fujiwara H.,
RA Fukui Y., Toshihiko A., Yamaguchi M., Kusumi T.;
RT "Molecular cloning and biochemical characterization of
RT hydroxycinnamoyl-CoA:anthocyanin 3-O-glucoside-6-O-
RT hydroxycinnamoyltransferase from Perilla frutescens and diverse plant
RT acyltransferase homologs."
RL Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB026495; BAA93451.1; -
DR InterPro: IPR003480; Transferase.
DR Pfam: PF02458; Transferase; 1.
KW TRANSFERASE.
SQ SEQUENCE 448 AA; 49919 MW; 85D8EECEDDC188C8 CRC64;

Query Match Best Local Similarity 100.0%; Score 40; DB 10; Length 448;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWK 6
Db 390 DFGWK 395

RESULT 11
ID Q9FTD1 PRELIMINARY; PRT: 448 AA.

AC Q9FTD1; 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE ANTHOCYANIN ACYLTRANSFERASE-LIKE PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=99156233; PubMed=10048488;
RA Asanizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VIII.
RT Sequence features of the regions of 1,081,958 bp covered by seventeen
RT physically assigned P1 and TAC clones."
RL DNA Res. 5:379-391(1998).
DR EMBL; AB016892; BAB10831.1; -
DR InterPro: IPR003480; Transferase.
DR Pfam: PF02458; Transferase; 1.

KW Transference: Acyltransferase.
SQ SEQUENCE 448 AA; 49916 MW; 27878BBE9BB984E CRC64;

Query Match 100.0%; Score 40; DB 10; Length 448;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWGK 6
DB 393 DFGWGK 398

RESULT 12
O9FH98 PRELIMINARY: PRT: 448 AA.
ID O9FH98;
AC O9FH98;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 17, Last sequence update)
DE ANTHRANILATE N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE-LIKE PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones."
RL DNA Res. 7:31-63(2000).
DR EMBL: AB020742; BAB10949.1; -
DR InterPro: IPR003480; Transferase.
DR Pfam: PF02458; Transferase; 1.
KW Transferase.
SQ SEQUENCE 448 AA; 49939 MW; 04EB676545093DEA CRC64;

Query Match 100.0%; Score 40; DB 10; Length 448;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DFGWGK 6
DB 389 DFGWGK 394

RESULT 13
O9LJB4 PRELIMINARY: PRT: 449 AA.
ID O9LJB4;
AC O9LJB4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ANTHOCYANIN 5-AROWATC ACYLTRANSFERASE-LIKE PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;

Px PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT TAC and BAC clones."
RL DNA Res. 7:217-221(2000).
DR EMBL: AP000606; BAB01191.1; -
DR InterPro: IPR003480; Transferase.
DR Pfam: PF02458; Transferase; 1.
KW Transferase; Acyltransferase.
SQ SEQUENCE 449 AA; 49439 MW; 2446D502AEC9D99B CRC64;

Query Match 100.0%; Score 40; DB 10; Length 449;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWGK 6
DB 394 DFGWGK 399

RESULT 14
O9SNE0 PRELIMINARY: PRT: 450 AA.
ID O9SNE0;
AC O9SNE0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ANTHRANILATE N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE-LIKE PROTEIN.
GN F1C1.110.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Barques M., Collado M.C., Navarro P., Terol J., Perez-Alonso M.,
RA Mewes H.W., Lemcke K., Mayer K.F.X., Queirer F., Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC EU Arabidopsis sequencing project;
RA Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AL132976; CAB62306.1; -
DR InterPro: IPR003480; Transferase.
DR Pfam: PF02458; Transferase; 1.
KW Transferase.
SQ SEQUENCE 450 AA; 49805 MW; 5D4A4AAAABCD3F0C6 CRC64;

Query Match 100.0%; Score 40; DB 10; Length 450;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWGK 6
DB 391 DFGWGK 396

RESULT 15
O64470 PRELIMINARY: PRT: 451 AA.
ID O64470;
AC O64470;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE PUTATIVE ANTHRANILATE N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE.
GN T20K24.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II: Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID-3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L.,
 RA Brandon R.C., Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D.,
 RA Somerville C.R., Venter J.C.,
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC002392; AAD12025.1; -
 DR InterPro; IPR003480; Transferase.
 DR Pfam; PF02458; Transferase; 1.
 KW Transferase
 SO SEQUENCE 451 AA; 50434 MW; B13B2CBF4DB4482 CRC64;

Query Match 100.0%; Score 40; DB 10; Length 451;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGWCK 6
 Db 397 DFGWCK 402

Search completed: November 5, 2001, 12:58:39
 Job time: 100 sec